

RAW SEQUENCE LISTING

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Application Serial Number: 101564,617
Source: TEUP
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/564,617

DATE: 01/30/2006
TIME: 14:44:31

Input Set : A:\2577-162.txt
Output Set: N:\CRF4\01302006\J564617.raw

3 <110> APPLICANT: Kwang , Jimmy
4 Ling, Ai Ee
5 Ooi, Eng Eong
6 Chng, Hiok Hee
8 <120> TITLE OF INVENTION: Diagnostics for SARS Virus
10 <130> FILE REFERENCE: 2577-162
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/564,617
C--> 12 <141> CURRENT FILING DATE: 2006-01-13
12 <150> PRIOR APPLICATION NUMBER: 60/486,918
13 <151> PRIOR FILING DATE: 2003-07-15
15 <150> PRIOR APPLICATION NUMBER: PCT/US04/003307
16 <151> PRIOR FILING DATE: 2004-02-04
18 <160> NUMBER OF SEQ ID NOS: 25
20 <170> SOFTWARE: PatentIn version 3.2
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1269
24 <212> TYPE: DNA
25 <213> ORGANISM: SARS coronavirus
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (1)..(1269)
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34 Met Ser Asp Asn Gly Pro Gln Ser Asn Gln Arg Ser Ala Pro Arg Ile
35 1 5 10 15
37 aca ttt ggt gga ccc aca gat tca act gac aat aac cag aat gga gga 96
38 Thr Phe Gly Gly Pro Thr Asp Ser Thr Asp Asn Asn Gln Asn Gly Gly
39 20 25 30
41 cgc aat ggg gca agg cca aaa cag cgc cga ccc caa ggt tta ccc aat 144
42 Arg Asn Gly Ala Arg Pro Lys Gln Arg Arg Pro Gln Gly Leu Pro Asn
43 35 40 45
45 aat act gcg tct tgg ttc aca gct ctc act cag cat ggc aag gag gaa 192
46 Asn Thr Ala Ser Trp Phe Thr Ala Leu Thr Gln His Gly Lys Glu Glu
47 50 55 60
49 ctt aga ttc cct cga ggc cag ggc gtt cca atc aac acc aat agt ggt 240
50 Leu Arg Phe Pro Arg Gly Gln Gly Val Pro Ile Asn Thr Asn Ser Gly
51 65 70 75 80
53 cca gat gac caa att ggc tac tac cga aga gct acc cga cga gtt cgt 288
54 Pro Asp Asp Gln Ile Gly Tyr Tyr Arg Arg Ala Thr Arg Arg Val Arg
55 85 90 95
57 ggt ggt gac ggc aaa atg aaa gag ctc agc ccc aga tgg tac ttc tat 336
58 Gly Gly Asp Gly Lys Met Lys Glu Leu Ser Pro Arg Trp Tyr Phe Tyr
59 100 105 110

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61 tac cta gga act ggc cca gaa gct tca ctt ccc tac ggc gct aac aaa	384
62 Tyr Leu Gly Thr Gly Pro Glu Ala Ser Leu Pro Tyr Gly Ala Asn Lys	
63 115 120 125	
65 gaa ggc atc gta tgg gtt gca act gag gga gcc ttg aat aca ccc aaa	432
66 Glu Gly Ile Val Trp Val Ala Thr Glu Gly Ala Leu Asn Thr Pro Lys	
67 130 135 140	
69 gac cac att ggc acc cgc aat cct aat aac aat gct gcc acc gtg cta	480
70 Asp His Ile Gly Thr Arg Asn Pro Asn Asn Ala Ala Thr Val Leu	
71 145 150 155 160	
73 caa ctt cct caa gga aca aca ttg cca aaa ggc ttc tac gca gag gga	528
74 Gln Leu Pro Gln Gly Thr Thr Leu Pro Lys Gly Phe Tyr Ala Glu Gly	
75 165 170 175	
77 agc aga ggc ggc agt caa gcc tct tct cgc tcc tca tca cgt agt cgc	576
78 Ser Arg Gly Gly Ser Gln Ala Ser Ser Arg Ser Ser Arg Ser Arg	
79 180 185 190	
81 ggt aat tca aga aat tca act cct ggc agc agt agg gga aat tct cct	624
82 Gly Asn Ser Arg Asn Ser Thr Pro Gly Ser Ser Arg Gly Asn Ser Pro	
83 195 200 205	
85 gct cga atg gct agc gga ggt ggt gaa act gcc ctc gcg cta ttg ctg	672
86 Ala Arg Met Ala Ser Gly Gly Glu Thr Ala Leu Ala Leu Leu	
87 210 215 220	
89 cta gac aga ttg aac cag ctt gag agc aaa gtt tct ggt aaa ggc caa	720
90 Leu Asp Arg Leu Asn Gln Leu Glu Ser Lys Val Ser Gly Lys Gln	
91 225 230 235 240	
93 caa caa caa ggc caa act gtc act aag aaa tct gct gct gag gca tct	768
94 Gln Gln Gln Gly Gln Thr Val Thr Lys Lys Ser Ala Ala Glu Ala Ser	
95 245 250 255	
97 aaa aag cct cgc caa aaa cgt act gcc aca aaa cag tac aac gtc act	816
98 Lys Lys Pro Arg Gln Lys Arg Thr Ala Thr Lys Gln Tyr Asn Val Thr	
99 260 265 270	
101 caa gca ttt ggg aga cgt ggt cca gaa caa acc caa gga aat ttc ggg	864
102 Gln Ala Phe Gly Arg Arg Gly Pro Glu Gln Thr Gln Gly Asn Phe Gly	
103 275 280 285	
105 gac caa gac cta atc aga caa gga act gat tac aaa cat tgg ccg caa	912
106 Asp Gln Asp Leu Ile Arg Gln Gly Thr Asp Tyr Lys His Trp Pro Gln	
107 290 295 300	
109 att gca caa ttt gct cca agt gcc tct gca ttc ttt gga atg tca cgc	960
110 Ile Ala Gln Phe Ala Pro Ser Ala Ser Ala Phe Phe Gly Met Ser Arg	
111 305 310 315 320	
113 att ggc atg gaa gtc aca cct tcg gga aca tgg ctg act tat cat gga	1008
114 Ile Gly Met Glu Val Thr Pro Ser Gly Thr Trp Leu Thr Tyr His Gly	
115 325 330 335	
117 gcc att aaa ttg gat gac aaa gat cca caa ttc aaa gac aac gtc ata	1056
118 Ala Ile Lys Leu Asp Asp Lys Asp Pro Gln Phe Lys Asp Asn Val Ile	
119 340 345 350	
121 ctg ctg aac aag cac att gac gca tac aaa aca ttc cca cca aca gag	1104
122 Leu Leu Asn Lys His Ile Asp Ala Tyr Lys Thr Phe Pro Pro Thr Glu	
123 355 360 365	
125 cct aaa aag gac aaa aag act gat gaa gct cag cct ttg ccg	1152

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126 Pro Lys Lys Asp Lys Lys Lys Lys Thr Asp Glu Ala Gln Pro Leu Pro
127 370 375 380
129 cag aga caa aag aag cag ccc act gtg act ctt ctt cct gcg gct gac 1200
130 Gln Arg Gln Lys Lys Gln Pro Thr Val Thr Leu Leu Pro Ala Ala Asp
131 385 390 395 400
133 atg gat gat ttc tcc aga caa ctt caa aat tcc atg agt gga gct tct 1248
134 Met Asp Asp Phe Ser Arg Gln Leu Gln Asn Ser Met Ser Gly Ala Ser
135 405 410 415
137 gct gat tca act cag gca taa 1269
138 Ala Asp Ser Thr Gln Ala
139 420
142 <210> SEQ ID NO: 2
143 <211> LENGTH: 422
144 <212> TYPE: PRT
145 <213> ORGANISM: SARS coronavirus
147 <400> SEQUENCE: 2
149 Met Ser Asp Asn Gly Pro Gln Ser Asn Gln Arg Ser Ala Pro Arg Ile
150 1 5 10 15
153 Thr Phe Gly Gly Pro Thr Asp Ser Thr Asp Asn Asn Gln Asn Gly Gly
154 20 25 30
157 Arg Asn Gly Ala Arg Pro Lys Gln Arg Arg Pro Gln Gly Leu Pro Asn
158 35 40 45
161 Asn Thr Ala Ser Trp Phe Thr Ala Leu Thr Gln His Gly Lys Glu Glu
162 50 55 60
165 Leu Arg Phe Pro Arg Gly Gln Gly Val Pro Ile Asn Thr Asn Ser Gly
166 65 70 75 80
169 Pro Asp Asp Gln Ile Gly Tyr Tyr Arg Arg Ala Thr Arg Arg Val Arg
170 85 90 95
173 Gly Gly Asp Gly Lys Met Lys Glu Leu Ser Pro Arg Trp Tyr Phe Tyr
174 100 105 110
177 Tyr Leu Gly Thr Gly Pro Glu Ala Ser Leu Pro Tyr Gly Ala Asn Lys
178 115 120 125
181 Glu Gly Ile Val Trp Val Ala Thr Glu Gly Ala Leu Asn Thr Pro Lys
182 130 135 140
185 Asp His Ile Gly Thr Arg Asn Pro Asn Asn Ala Ala Thr Val Leu
186 145 150 155 160
189 Gln Leu Pro Gln Gly Thr Thr Leu Pro Lys Gly Phe Tyr Ala Glu Gly
190 165 170 175
193 Ser Arg Gly Gly Ser Gln Ala Ser Ser Arg Ser Ser Arg Ser Arg
194 180 185 190
197 Gly Asn Ser Arg Asn Ser Thr Pro Gly Ser Ser Arg Gly Asn Ser Pro
198 195 200 205
201 Ala Arg Met Ala Ser Gly Gly Glu Thr Ala Leu Ala Leu Leu Leu
202 210 215 220
205 Leu Asp Arg Leu Asn Gln Leu Glu Ser Lys Val Ser Gly Lys Gly Gln
206 225 230 235 240
209 Gln Gln Gln Gly Gln Thr Val Thr Lys Lys Ser Ala Ala Glu Ala Ser
210 245 250 255
213 Lys Lys Pro Arg Gln Lys Arg Thr Ala Thr Lys Gln Tyr Asn Val Thr

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214	260	265	270	
217 Gln Ala Phe Gly Arg Arg Gly Pro Glu Gln Thr Gln Gly Asn Phe Gly				
218 275	280	285		
221 Asp Gln Asp Leu Ile Arg Gln Gly Thr Asp Tyr Lys His Trp Pro Gln				
222 290	295	300		
225 Ile Ala Gln Phe Ala Pro Ser Ala Ser Ala Phe Phe Gly Met Ser Arg				
226 305	310	315	320	
229 Ile Gly Met Glu Val Thr Pro Ser Gly Thr Trp Leu Thr Tyr His Gly				
230 325	330	335		
233 Ala Ile Lys Leu Asp Asp Lys Asp Pro Gln Phe Lys Asp Asn Val Ile				
234 340	345	350		
237 Leu Leu Asn Lys His Ile Asp Ala Tyr Lys Thr Phe Pro Pro Thr Glu				
238 355	360	365		
241 Pro Lys Lys Asp Lys Lys Lys Thr Asp Glu Ala Gln Pro Leu Pro				
242 370	375	380		
245 Gln Arg Gln Lys Lys Gln Pro Thr Val Thr Leu Leu Pro Ala Ala Asp				
246 385	390	395	400	
249 Met Asp Asp Phe Ser Arg Gln Leu Gln Asn Ser Met Ser Gly Ala Ser				
250 405	410	415		
253 Ala Asp Ser Thr Gln Ala				
254 420				
257 <210> SEQ ID NO: 3				
258 <211> LENGTH: 3768				
259 <212> TYPE: DNA				
260 <213> ORGANISM: SARS coronavirus				
263 <220> FEATURE:				
264 <221> NAME/KEY: CDS				
265 <222> LOCATION: (1)..(3768)				
267 <400> SEQUENCE: 3				
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269 Met Phe Ile Phe Leu Leu Phe Leu Thr Leu Thr Ser Gly Ser Asp Leu				
270 1 5 10 15				
272 gac cgg tgc acc act ttt gat gat gtt caa gct cct aat tac act caa				96
273 Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln				
274 20 25 30				
276 cat act tca tct atg agg ggg gtt tac tat cct gat gaa att ttt aga				144
277 His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg				
278 35 40 45				
280 tca gac act ctt tat tta act cag gat tta ttt ctt cca ttt tat tct				192
281 Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser				
282 50 55 60				
284 aat gtt aca ggg ttt cat act att aat cat acg ttt ggc aac cct gtc				240
285 Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val				
286 65 70 75 80				
288 ata cct ttt aag gat ggt att tat ttt gct gcc aca gag aaa tca aat				288
289 Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn				
290 85 90 95				
292 gtt gtc cgt ggt tgg gtt ttt ggt tct acc atg aac aac aag tca cag				
293 Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln				336

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294	100	105	110	
296	tcg gtg att att aac aat tct act aat gtt gtt ata cga gca tgt			384
297	Ser Val Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys			
298	115	120	125	
300	aac ttt gaa ttg tgt gac aac cct ttc ttt gct gtt tct aaa ccc atg			432
301	Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met			
302	130	135	140	
304	ggt aca cag aca cat act atg ata ttc gat aat gca ttt aat tgc act			480
305	Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn Ala Phe Asn Cys Thr			
306	145	150	155	160
308	ttc gag tac ata tct gat gcc ttt tcg ctt gat gtt tca gaa aag tca			
309	Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp Val Ser Glu Lys Ser			
310	165	170	175	
312	ggt aat ttt aaa cac tta cga gag ttt gtg ttt aaa aat aaa gat ggg			576
313	Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe Lys Asn Lys Asp Gly			
314	180	185	190	
316	ttt ctc tat gtt tat aag ggc tat caa cct ata gat gta gtt cgt gat			624
317	Phe Leu Tyr Val Tyr Lys Gly Tyr Gln Pro Ile Asp Val Val Arg Asp			
318	195	200	205	
320	cta cct tct ggt ttt aac act ttg aaa cct att ttt aag ttg cct ctt			672
321	Leu Pro Ser Gly Phe Asn Thr Leu Lys Pro Ile Phe Lys Leu Pro Leu			
322	210	215	220	
324	ggt att aac att aca aat ttt aga gcc att ctt aca gcc ttt tca cct			720
325	Gly Ile Asn Ile Thr Asn Phe Arg Ala Ile Leu Thr Ala Phe Ser Pro			
326	225	230	235	240
328	gct caa gac att tgg ggc acg tca gct gca gcc tat ttt gtt ggc tat			768
329	Ala Gln Asp Ile Trp Gly Thr Ser Ala Ala Ala Tyr Phe Val Gly Tyr			
330	245	250	255	
332	tta aag cca act aca ttt atg ctc aag tat gat gaa aat ggt aca atc			816
333	Leu Lys Pro Thr Thr Phe Met Leu Lys Tyr Asp Glu Asn Gly Thr Ile			
334	260	265	270	
336	aca gat gct gtt gat tgt tct caa aat cca ctt gct gaa ctc aaa tgc			864
337	Thr Asp Ala Val Asp Cys Ser Gln Asn Pro Leu Ala Glu Leu Lys Cys			
338	275	280	285	
340	tct gtt aag agc ttt gag att gac aaa gga att tac cag acc tct aat			912
341	Ser Val Lys Ser Phe Glu Ile Asp Lys Gly Ile Tyr Gln Thr Ser Asn			
342	290	295	300	
344	ttc agg gtt gtt ccc tca gga gat gtt gtg aga ttc cct aat att aca			960
345	Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe Pro Asn Ile Thr			
346	305	310	315	320
348	aac ttg tgt cct ttt gga gag gtt ttt aat gct act aaa ttc cct tct			1008
349	Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Lys Phe Pro Ser			
350	325	330	335	
352	gtc tat gca tgg gag aga aaa aaa att tct aat tgt gtt gct gat tac			1056
353	Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala Asp Tyr			
354	340	345	350	
356	tct gtg ctc tac aac tca aca ttt ttc tca acc ttt aag tgc tat ggc			1104
357	Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Thr Phe Lys Cys Tyr Gly			
358	355	360	365	

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date